



1
SEQUENCE LISTING

GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Max-Planck-Gesellschaft zur Förderung der
Wissenschaften e.V.
(B) STREET: none
(C) CITY: Berlin
(D) STATE: none
(E) COUNTRY: Germany
(F) POSTAL CODE (ZIP): none

- (A) NAME: National Public Health Institute
(B) STREET: Mannerheimintie 166
(C) CITY: Helsinki
(D) STATE: none
(E) COUNTRY: Finland
(F) POSTAL CODE (ZIP): 00300

(ii) TITLE OF INVENTION: Novel nucleic acid molecule encoding a
(poly)peptide co-segregating in mutated form with
Autoimmune Polyendocrinopathy Candidiasis Ectodermal
Dystrophy (APECED)

(iii) NUMBER OF SEQUENCES: 32

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGGCGCACA GCCGGCGCGG AGGCCCCACA GCCCCGCCGG GACCCGAGGC CAAGCGAGGG 60
GCTGCCAGTG TCCCGGGACC CACCGCGTCC GCCCCAGCCC CGGGTCCCCG CGCCACCCCC 120
ATGGCGACGG ACGCGGCGCT ACGCCGGCTT CTGAGGCTGC ACCGCACGGA GATCGCGGTG 180
GCCGTGGACA GCGCCTTCCC ACTGCTGCAC GCGCTGGCTG ACCACGACGT GGTCCCCGAG 240
GACAAGTTTC AGGAGACGCT TCATCTGAAG GAAAAGGAGG GCTGCCCCCA GGCCTTCCAC 300
GCCCTCCTGT CCTGGCTGCT GACCCAGGAC TCCACAGCCA TCCTGGACTT CTGGAGGGTG 360

CTGTTCAAGG ACTACAACCT GGAGCGCTAT GGCCGGCTGC AGCCCATCCT GGACAGCTTC 420
 CCCAAAGATG TGGACCTCAG CCAGCCCCGG AAGGGGAGGA AGCCCCCGGC CGTCCCCAAG 480
 GCTTTGGTAC CGCCACCCAG ACTCCCCACC AAGAGGAAGG CCTCAGAAGA GGCTCGAGCT 540
 GCCGCGCCAG CAGCCCTGAC TCCAAGGGGC ACCGCCAGCC CAGGCTCTCA ACTGAAGGCC 600
 AAGCCCCCA AGAAGCCGGA GAGCAGCGCA GAGCAGCAGC GCCTTCCACT CGGGAACGGG 660
 ATTCAGACCA TGTCAGCTTC AGTCCAGAGA GCTGTGGCCA TGTCTCCGG GGACGTCCCG 720
 GGAGCCCGAG GGGCCGTGGA GGGGATCCTC ATCCAGCAGG TGTTTGAGTC AGGCGGCTCC 780
 AAGAAGTGCA TCCAGGTTGG TGGGGAGTTC TACTCTCCA GCAAGTTCGA AGACTCCGGC 840
 AGTGGGAAGA ACAAGGCCCG CAGCAGCAGT GGCCCGAAGC CTCTGGTTCTG AGCCAAGGGA 900
 GCCCAGGGCG CTGCCCCCGG TGGAGGTGAG GCTAGGCTGG GCCAGCAGGG CAGCGTTCCC 960
 GCCCCTCTGG CCCTCCCCAG TGACCCCCAG CTCCACCAGA AGAATGAGGA CGAGTGTGCC 1020
 GTGTGTCGGG ACGGCGGGGA GCTCATCTGC TGTGACGGCT GCCCTCGGGC CTTCCACCTG 1080
 GCCTGCCTGT CCCCTCCGCT CCGGGAGATC CCCAGTGGGA CCTGGAGGTG CTCCAGCTGC 1140
 CTGCAGGCAA CAGTCCAGGA GGTGCAGCCC CGGGCAGAGG AGCCCCGGCC CCAGGAGCCA 1200
 CCCGTGGAGA CCCCGCTCCC CCCGGGGCTT AGGTCGGCGG GAGAGGAGGT AAGAGGTCCA 1260
 CCTGGGGAAC CCCTAGCCGG CATGGACACG ACTCTTGTCT ACAAGCACCT GCCGGCTCCG 1320
 CCTTCTGCAG CCCCGCTGCC AGGGCTGGAC TCCTCGGGCC TGCACCCCT ACTGTGTGTG 1380
 GGTCTGAGG GTCAGCAGAA CCTGGCTCCT GGTGCGCGTT GCGGGGTGTG CGGAGATGGT 1440
 ACGGACGTGC TGCGGTGTAC TACTGCGCC GCTGCCTTTC ACTGGCGCTG CCACTTCCCA 1500
 GCCGGCACCT CCCGGCCCCG GACGGGCCTG CGCTGCAGAT CCGTCTCAGG AGACGTGACC 1560
 CCAGCCCCTG TGGAGGGGGT GCTGGCCCCC AGCCCCGCCC GCCTGGCCCC TGGGCCTGCC 1620
 AAGGATGACA CTGCCAGTCA CGAGCCCGCT CTGCACAGGG ATGACCTGGA GTCCCTTCTG 1680
 AGCGAGCACA CCTTCGATGG CATCCTGCAG TGGGCCATCC AGAGCATGGC CCGTCCGGCG 1740
 GCCCCCTTCC CCTCCTGACC CCAGATGGCC GGGACATGCA GCTCTGATGA GAGAGTGCTG 1800
 AGAAGGACAC CTCCTTCCTC AGTCCTGGAA GCCGGCCGGC TGGGATCAAG AAGGGGACAG 1860
 CGCCACCTCT TGTCAGTGCT CGGCTGTAAA CAGCTCTGTG TTTCTGGGGA CACCAGCCAT 1920
 CATGTGCCTG GAAATTAAAC CCTGCCCCAC TTCTCTACTC TGAAGTCCC CGGAGCCTC 1980
 TCCTTGCTG GTGACCTACT AAAAATATAA AAATTAGCTG GGTGTGGTGG TGGGTGCCTG 2040
 TAATCCCAGC TACATGGGAG CCTGAGGCAT GAGAATCACT TGAACCTGGG AGGTGGAGGT 2100
 TGCAGTGAGC TGAGATTGCG CCACTGCACT CCAGTCTGGT CGGCAAGAGT GAGACTCCGT 2160
 CTCAAAAACA AAACAAAAAA ACCACATAAC ATAAATTTAT CATCTCGACC ACTTTTCAGT 2220

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TCAGTGGCAT TCACATCTCA TGTA

2245

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
 1 5 10 15
 Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
 20 25 30
 Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
 35 40 45
 Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
 50 55 60
 Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
 65 70 75 80
 Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
 85 90 95
 Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
 100 105 110
 Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
 115 120 125
 Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
 130 135 140
 Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
 145 150 155 160
 Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
 165 170 175
 Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
 180 185 190
 Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
 195 200 205
 Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
 210 215 220
 Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly

225 230 235 240
 Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
 245 250 255

 Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
 260 265 270

 Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
 275 280 285

 Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
 290 295 300

 Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
 305 310 315 320

 Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
 325 330 335

 Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
 340 345 350

 Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
 355 360 365

 Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
 370 375 380

 Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
 385 390 395 400

 Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
 405 410 415

 Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
 420 425 430

 Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
 435 440 445

 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
 450 455 460

 Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
 465 470 475 480

 Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
 485 490 495

 Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
 500 505 510

 Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
 515 520 525

 Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
 530 535 540

 Ser

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 nk

545

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ACAGGCAGGC AG

12

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACAGGCAGGC CA

12

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCAGGCCAGG TG

12

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGGAGGGGA CA

12

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTGTGGACTG TCACGGAAAC CCCACGTGT GATGGAAAGT CCAAAATTCT ACAGGAGTCT

60

TTCTGTTGAT CTCCAGTCAG AGGCTGGGGG

90

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AAGGGGCTGG TGTGGAAAGC CCCACGGCAT GGTGGAAAGT CCGAAATTCT ACAGGGGCCT

60

CTTTGTAAAA CCTCCATGCA AGAGGCTGGG

90

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

NNGNGGNNG TNNNGNAANC CCCNNNGNNT GNTGGAAAGT CCNAAATTCT ACAGGNGNCT 60
 NTNTGTTNAN CNNC NNTNNN AGNNNNNGGG 90

N represents any nucleotide or a gap

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATGGCAGGTG GGGATGGAAT GCTACGCCGT CTGCTGAGGC TGCACCGCAC CGAGATCGCG 60
 GTGGCCATAG ACAGTGCCTT TCCGCTGCTG CATGCTCTAG CCGACCACGA CGTGGTCCCT 120
 GAGGACAAGT TCCAGGAGAC GCTCCGTCTG AAGGAGAAGG AAGGCTGCCC CCAGGCCTTC 180
 CACGCCCTGC TGTCTGGCT CCTGACCCGG GACAGTGGGG CCATCCTGGA TTTCTGGAGG 240
 ATTCTCTTTA AGGACTACAA TCTGGAGCGG TACAGCCGCC TGCATAGCAT CCTGGACGGC 300
 TTCCCAAAG ATGTGGACCT AAACCAGTCC CGGAAAGGGA GAAAGCCCCT TGCTGGTCCC 360
 AAGGCCGCGG TACTGCCACC CAGACCCCCC ACCAAGAGAA AAGCACTGGA GGAGCCTCGA 420
 GCCACCCAC CAGCAACTCT GGCTCAAAG AGCGTCTCCA GCCCAGGCTC CCACCTGAAG 480
 ACTAAGCCCC CTAAGAAGCC AGATGGCAAC TTGGAGTCAC AGCACCTTCC TCTTGAAAC 540
 GGAATTCAGA CCATGGCAGC TTCTGTCCAG AGAGCTGTGA CCGTGGCCTC TGGGGATGTT 600
 CCAGGAACCC GAGGGGCCGT GGAAGGGATC CTTATCCAGC AGGTGTTTGA GTCAGGAAGA 660
 TCCAAGAAGT GCATTCAGGT TGGGGGAGAG TTTTATACAC CCAACAAGTT CGAAGACCCC 720
 AGTGGCAATT TGAAGAACAA GGCCCGGAGT GGTAGCAGCC TAAAGCCAGT GGTCCGAGCC 780
 AAGGGAGCCC AGGTCACTAT ACCTGGTAGA GATGAGCAGA AAGTGGGCCA GCAGTGTGGG 840
 GTTCCTCCCC TTCCATCCCT CCCAGTGAG CCCAGGTTA ACCAGAAGAA CGAGGATGAG 900
 TGTGCCGTGT GCCACGACGG AGGTGAGCTC ATCTGTTGTG ACGGCTGTCC CCGGGCCTTC 960
 CACCTGGCTT GCCTGTCCCC ACCTCTGCAG GAGATCCCCA GTGGCCTCTG GAGATGCTCC 1020
 TGCTGCCTCC AGGGCAGAGT CCAACAGAAC CTGTCCCAGC CTGAGGTGTC CAGGCCCCCG 1080
 GAGCTACCTG CAGAGACCCC GATCCTCGTG GGACTGAGGT CAGCTTCAGA GAAAACCAGG 1140

GGCCCATCCA GGGAGCTCAA AGCCAGCTCT GATGCTGCTG TCACATATGT GAACCTGCTG 1200
 GCGCCGACCC CTGCAGCTCC TCTGCTGGAG CCTTCAGCAC TGTGCCCTCT ACTGAGTGCT 1260
 GCGAATGAGG GCGCGCCAGG TCCAGCACCA AGCGCGCGAT GCAGTGTGTG TGGCGATGGC 1320
 ACCGAGGTGT TCGGGTGTGC ACACGTGTGCC GCTGCCTTCC ACTGGCGCTG CCACTTCCCG 1380
 ACGGCCGCCG CCGGCCGGG GACCAATCTC CGCTGCAAAT CCTGCTCTGC AGACTCGACT 1440
 CCCACGCCAG GCACACCGGG CGAAGCTGTA CCCACCTCTG GGCCCCGTCC AGCACCTGGG 1500
 CTTGCCAAGG TAGGGGACGA CTCTGCTAGT CACGACCCTG TTCTACATAG GGACGACCTG 1560
 GAGTCCCTCC TCAATGAGCA CTCATTTGAC GGCATCCTGC AGTGGGCCAT CCAGAGCATG 1620
 TCACGCCCCG TGGCCGAGAC ACCACCCTTC TCTTCCTGA 1659

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
 1 5 10 15
 Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
 20 25 30
 Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
 35 40 45
 Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
 50 55 60
 Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
 65 70 75 80
 Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
 85 90 95
 Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
 100 105 110
 Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
 115 120 125
 Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
 130 135 140
 Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
 145 150 155 160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
 165 170 175
 Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
 180 185 190
 Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
 195 200 205
 Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
 210 215 220
 Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
 225 230 235 240
 Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
 245 250 255
 Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
 260 265 270
 Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
 275 280 285
 Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
 290 295 300
 His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
 305 310 315 320
 His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
 325 330 335
 Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
 340 345 350
 Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
 355 360 365
 Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
 370 375 380
 Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
 385 390 395 400
 Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
 405 410 415
 Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
 420 425 430
 Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
 435 440 445
 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
 450 455 460
 Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
 465 470 475 480

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Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
485 490 495

Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
500 505 510

Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
515 520 525

Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
530 535 540

Ala Glu Thr Pro Pro Phe Ser Ser
545 550

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1 5 10 15

Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
20 25 30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
50 55 60

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
85 90 95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
100 105 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
145 150 155 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
165 170 175

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Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
 180 185 190
 Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
 195 200 205
 Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
 210 215 220
 Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
 225 230 235 240
 Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
 245 250 255
 Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
 260 265 270
 Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
 275 280 285
 Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
 290 295 300
 Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
 305 310 315 320
 Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
 325 330 335
 Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
 340 345 350
 Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
 355 360 365
 Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
 370 375 380
 Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
 385 390 395 400
 Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
 405 410 415
 Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
 420 425 430
 Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
 435 440 445
 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
 450 455 460
 Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
 465 470 475 480
 Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
 485 490 495

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Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
 500 505 510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
 515 520 525

Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
 530 535 540

Ser
 545

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg
 1 5 10 15

Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala
 20 25 30

Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu
 35 40 45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu
 50 55 60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg
 65 70 75 80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser
 85 90 95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys
 100 105 110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg
 115 120 125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro
 130 135 140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys
 145 150 155 160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu
 165 170 175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala
 180 185 190
 Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu
 195 200 205
 Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys
 210 215 220
 Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro
 225 230 235 240
 Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro
 245 250 255
 Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu
 260 265 270
 Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro
 275 280 285
 Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys
 290 295 300
 His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe
 305 310 315 320
 His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu
 325 330 335
 Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser
 340 345 350
 Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile
 355 360 365
 Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg
 370 375 380
 Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu
 385 390 395 400
 Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro
 405 410 415
 Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala
 420 425 430
 Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His
 435 440 445
 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala
 450 455 460
 Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr
 465 470 475 480
 Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg
 485 490 495

Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp
 500 505 510

Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser
 515 520 525

Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu
 530 535 540

Ala Glu Thr Pro Pro Phe Ser Ser
 545 550

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Xaa Xaa Asp Xaa Xaa Leu Arg Arg Leu Leu Arg Leu His Arg Thr
 1 5 10 15

Glu Ile Ala Val Ala Xaa Asp Ser Ala Phe Pro Leu Leu His Ala Leu
 20 25 30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu Xaa
 35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
 50 55 60

Trp Leu Leu Thr Xaa Asp Ser Xaa Ala Ile Leu Asp Phe Trp Arg Xaa
 65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Xaa Arg Leu Xaa Xaa Ile
 85 90 95

Leu Asp Xaa Phe Pro Lys Asp Val Asp Leu Xaa Gln Xaa Arg Lys Gly
 100 105 110

Arg Lys Pro Xaa Ala Xaa Pro Lys Ala Xaa Val Xaa Pro Pro Arg Xaa
 115 120 125

Pro Thr Lys Arg Lys Ala Xaa Glu Glu Xaa Arg Ala Xaa Xaa Pro Ala
 130 135 140

Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Gly Ser Xaa Leu Lys Xaa
 145 150 155 160

Lys Pro Pro Lys Lys Pro Xaa Xaa Xaa Xaa Glu Xaa Gln Xaa Leu Pro
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Xaa Ala Ser Val Gln Arg Ala Val
 180 185 190
 Xaa Xaa Xaa Ser Gly Asp Val Pro Gly Xaa Arg Gly Ala Val Glu Gly
 195 200 205
 Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Xaa Ser Lys Lys Cys Ile
 210 215 220
 Gln Val Gly Gly Glu Phe Tyr Thr Pro Xaa Lys Phe Glu Asp Xaa Ser
 225 230 235 240
 Gly Xaa Xaa Lys Asn Lys Ala Arg Ser Xaa Ser Xaa Xaa Lys Pro Xaa
 245 250 255
 Val Arg Ala Lys Gly Ala Gln Xaa Xaa Xaa Pro Gly Xaa Xaa Glu Xaa
 260 265 270
 Xaa Xaa Gly Gln Gln Xaa Xaa Val Pro Xaa Xaa Xaa Xaa Leu Pro Ser
 275 280 285
 Xaa Pro Gln Xaa Xaa Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Xaa
 290 295 300
 Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His
 305 310 315 320
 Leu Ala Cys Leu Ser Pro Pro Leu Xaa Glu Ile Pro Ser Gly Xaa Trp
 325 330 335
 Arg Cys Ser Xaa Cys Leu Gln Xaa Xaa Val Gln Xaa Xaa Xaa Xaa Xaa
 340 345 350
 Xaa Glu Xaa Xaa Arg Pro Xaa Glu Xaa Pro Xaa Glu Thr Pro Xaa Xaa
 355 360 365
 Xaa Gly Leu Arg Ser Ala Xaa Glu Xaa Xaa Arg Gly Pro Xaa Xaa Glu
 370 375 380
 Xaa Xaa Ala Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Xaa Xaa Leu Xaa Ala
 385 390 395 400
 Pro Xaa Xaa Ala Ala Pro Leu Xaa Xaa Leu Xaa Xaa Ser Ala Leu Xaa
 405 410 415
 Pro Leu Leu Xaa Xaa Gly Xaa Glu Gly Xaa Xaa Xaa Xaa Ala Pro Xaa
 420 425 430
 Ala Arg Cys Xaa Val Cys Gly Asp Gly Thr Xaa Val Leu Arg Cys Xaa
 435 440 445
 His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Xaa Xaa Xaa
 450 455 460
 Xaa Arg Pro Gly Thr Xaa Leu Arg Cys Xaa Ser Cys Ser Xaa Asp Xaa
 465 470 475 480
 Thr Pro Xaa Pro Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Ser Xaa Xaa
 485 490 495

Bl
 wj

Arg Xaa Ala Pro Gly Xaa Ala Lys Xaa Xaa Asp Asp Xaa Ala Ser His
500 505 510

Xaa Pro Xaa Leu His Arg Asp Asp Leu Glu Ser Leu Leu Xaa Glu His
515 520 525

Xaa Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Xaa Arg Pro
530 535 540

Xaa Ala Xaa Xaa Pro Xaa
545 550

Xaa denotes any amino acid

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGGGCCTCGA TGGACGTCTC TGGGGCCCAG GTCGTGGTTC GCGCGCTA

48

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Pro Glu Leu Pro Ala Glu Thr Pro Gly Pro Ala Pro Ser Ala Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AGTGAGCCCC AGGTTAACCA GAACGAGGAT GAGTGTGCCG TGT

43

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ser Glu Pro Gln Val Asn Gln Asn Glu Asp Glu Cys Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTACACCAGGC TCGGTTCCCT CGGGTCCCAT CTCTACTCGT CTTTCACC

48

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Val Arg Ala Lys Gly Ala Gln Gly Arg Asp Glu Gln Lys Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGAAGTGCAT CCAGGTTGGC

20

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGAAGAGGGG CGTCAGCAAT

20

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met	Ala	Thr	Asp	Ala	Ala	Leu	Arg	Arg	Leu	Leu	Arg	Leu	His	Arg
1						5			10				15	

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ser Gln Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gly Gly Cys Thr Thr Cys Thr Gly Ala Gly Gly Cys Thr Gly Cys Ala
1 5 10 15
Cys Cys

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GCTCTGGATG GCCTACTGC

19

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AGAAGTGCAT CCAGGTTGGC

20

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GTGTGCTCGC TCAGAAGGG

19

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TGGCAGGTGG GGATGGAA

18

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GGAGGGATGG AAGGGGAGGA

20

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES


(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TCCCACCTGA AGACTAAGC

19

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- 
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TCACAGCTCT CTGGACAGAA

20

1

1